Análisis Inteligente de Datos: Segundo Parcial

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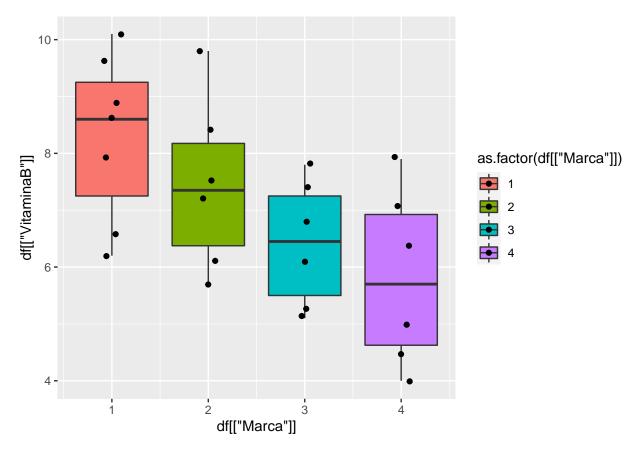
04 de mayo de 2022

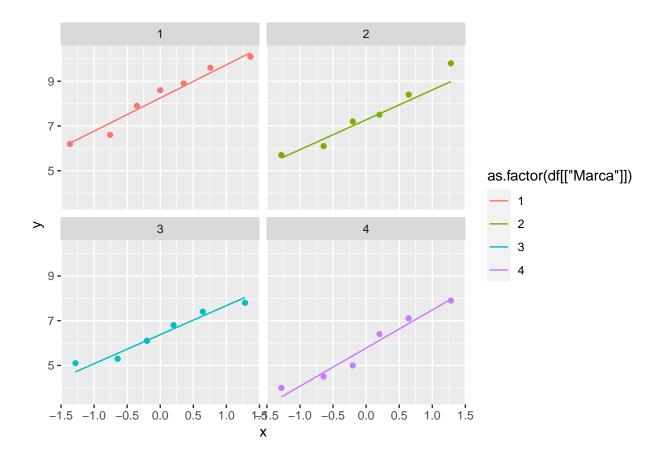
Intro ANOVA

Datos

```
## spec_tbl_df [25 x 2] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
## $ VitaminaB: num [1:25] 7.9 6.2 6.6 8.6 8.9 10.1 9.6 5.7 7.5 9.8 ...
              : num [1:25] 1 1 1 1 1 1 1 2 2 2 ...
## $ Marca
##
   - attr(*, "spec")=
    .. cols(
##
##
          VitaminaB = col_double(),
##
          Marca = col_double()
##
    ..)
  - attr(*, "problems")=<externalptr>
## # A tibble: 0 x 0
Head:
## # A tibble: 6 x 2
   VitaminaB Marca
##
         <dbl> <dbl>
          7.9
## 1
## 2
           6.2
## 3
           6.6
## 4
           8.6
                   1
## 5
           8.9
                   1
          10.1
## 6
                   1
Observaciones por grupo:
## # A tibble: 4 x 2
   `df[["Marca"]]` `n()`
##
##
               <dbl> <int>
## 1
                   1
## 2
                   2
                         6
## 3
                   3
                         6
## 4
```

Se cumplen los supuestos para su implementación?





Anova

```
## [1] 7.9 6.2 6.6 8.6 8.9 10.1 9.6 5.7 7.5 9.8 6.1 8.4 7.2 6.8 7.8 ## [16] 5.1 7.4 5.3 6.1 6.4 7.1 7.9 4.5 5.0 4.0 ## [1] 1 1 1 1 1 1 2 2 2 2 2 2 3 3 3 3 3 3 4 4 4 4 4 4 ## Levels: 1 2 3 4
```

fit del modelo

##

```
## fact    3    22.93    7.645    3.791 0.0256 *
## Residuals    21    42.35    2.016
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

Df Sum Sq Mean Sq F value Pr(>F)

coeficientes

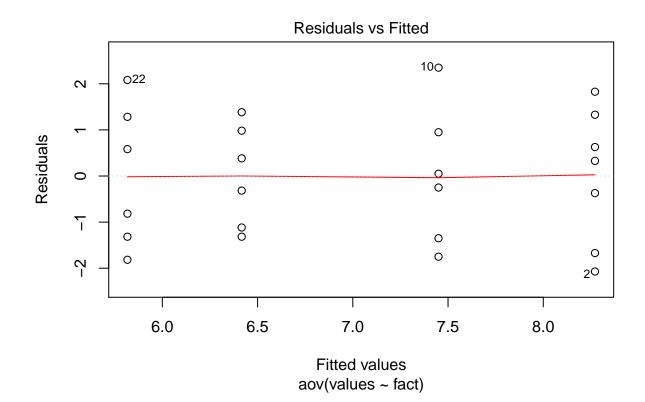
```
## (Intercept) fact2 fact3 fact4
## 8.2714286 -0.8214286 -1.8547619 -2.4547619
```

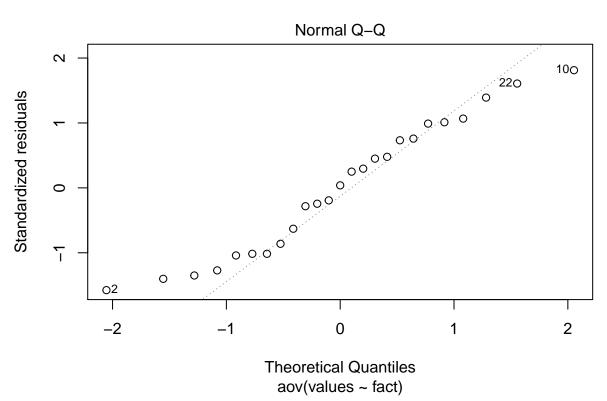
p-value

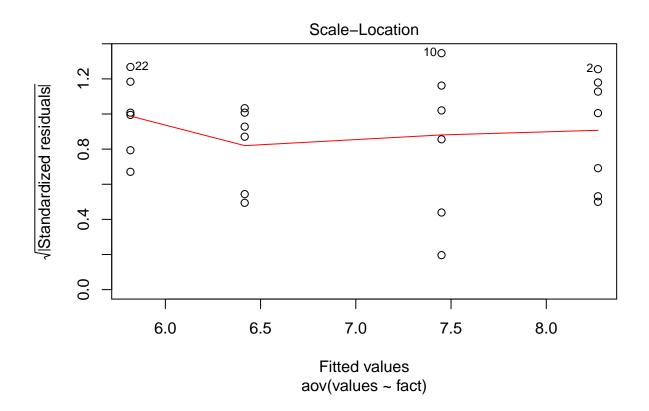
[1] 0.02563266

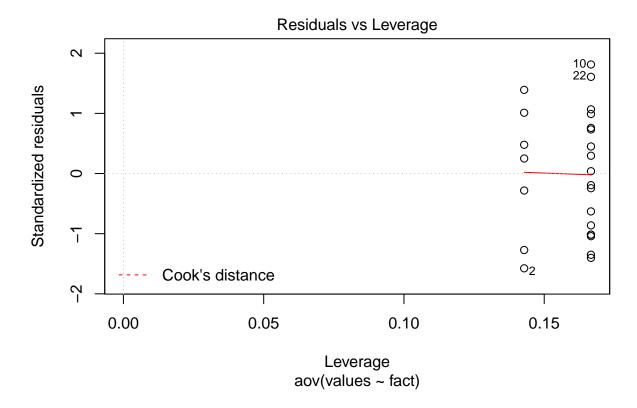
F-value

[1] 3.791114









Conclusión

[1] "HO debe rechazarse, al menos dos medias son distintas a nivel de significancia 0.05"

Testear homosedasticidad

```
Test de Levene
```

```
que no es sensible a la falta de normalidad o a la presencia de valores atípicos
```

```
## Levene's Test for Homogeneity of Variance (center = "median")
## Df F value Pr(>F)
## group 3 0.2949 0.8286
## 21
## [1] "No hay evidencia para rechazar HO, luego los datos son homosedásticos"
Test de Bartlett
sensibilidad al supuesto de normalidad
....
```

Testear normalidad

```
##
## Shapiro-Wilk normality test
##
## data: residuals(df_anova)
## W = 0.95307, p-value = 0.2937
## [1] "No hay evidencia para rechazar HO, luego los datos son normales"
```

Testear normalidad analizando residuos

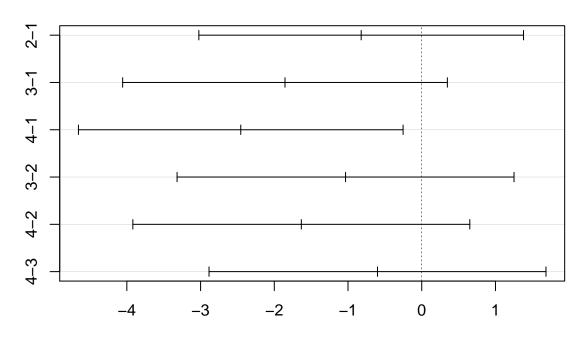
```
##
## Anderson-Darling normality test
##
## data: residuals(df_anova)
## A = 0.36947, p-value = 0.3995
## [1] "No hay evidencia para rechazar HO, luego los datos son normales"
##
## D'Agostino skewness test
##
## data: residuals(df_anova)
## skew = 0.065564, z = 0.159996, p-value = 0.8729
## alternative hypothesis: data have a skewness
## [1] "No hay evidencia para rechazar HO, luego los datos son normales"
```

Anova y después: post-hoc

Tukey's Honest Significant Differences (HSD)

```
##
     Tukey multiple comparisons of means
##
       95% family-wise confidence level
## Fit: aov(formula = values ~ fact, data = df)
## $fact
             diff
                        lwr
                                           p adj
                                   upr
## 2-1 -0.8214286 -3.023500 1.3806433 0.7284998
## 3-1 -1.8547619 -4.056834 0.3473100 0.1190380
## 4-1 -2.4547619 -4.656834 -0.2526900 0.0253506
## 3-2 -1.0333333 -3.318531 1.2518647 0.5969955
## 4-2 -1.6333333 -3.918531 0.6518647 0.2225040
## 4-3 -0.6000000 -2.885198 1.6851980 0.8832095
```

95% family-wise confidence level



Differences in mean levels of fact

Cuando ANOVA no funciona: test de Kruskal-Wallis

```
##
##
   Kruskal-Wallis rank sum test
##
## data: values by fact
## Kruskal-Wallis chi-squared = 7.9977, df = 3, p-value = 0.04606
## [1] "HO debe rechazarse: se encuentra significancia en la diferencia de al menos dos grupos"
## Multiple comparison test after Kruskal-Wallis
## p.value: 0.05
## Comparisons
##
         obs.dif critical.dif difference
## 1-2
        3.916667
                     10.80265
                                   FALSE
## 1-3 8.416667
                     10.80265
                                   FALSE
## 1-4 10.583333
                     10.80265
                                   FALSE
## 2-3 4.500000
                     11.21044
                                   FALSE
                                   FALSE
## 2-4 6.66667
                     11.21044
## 3-4 2.166667
                     11.21044
                                   FALSE
```

Analisis Discriminante Lineal (LDA)